



SEQUENCE LISTING

<110> Holloway, James L.

Lok, Si

Jaspers, Stephen R.

<120> Insulin Homolog Polypeptide Zins4

<130> 00-18

<150> US 60/188,544

<151> 2000-03-10

<160> 13

<170> FastSEQ for Windows Version 4.0

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AUG 20 2003

TECH CENTER 1600/2900

<210> 1

<211> 429

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(429)

<400> 1

atg gcc agg tac atg ctg ctg ctc ctg gcg gta tgg gtg ctg acc
Met Ala Arg Tyr Met Leu Leu Leu Leu Ala Val Trp Val Leu Thr
1 5 10 15

48

ggg gag ctg tgg ccg gga gct gag gcc cg^g gca g^g g^g cct tac ggg gtc
Gly Glu Leu Trp Pro Gly Ala Glu Ala Arg Ala Ala Pro Tyr Gly Val
20 25 30

96

agg ctt tgc ggc cga gaa ttc atc cga gca gtc atc ttc acc tgc ggg
Arg Leu Cys Gly Arg Glu Phe Ile Arg Ala Val Ile Phe Thr Cys Gly
35 40 45

144

ggc tcc cgg tgg aga cga tca gac atc ctg gcc cac gag gct atg gga
Gly Ser Arg Trp Arg Arg Ser Asp Ile Leu Ala His Glu Ala Met Gly
50 55 60

192

gat acc ttc ccg gat gca gat gct gat gaa gac agt ctg gca ggc gag	240
Asp Thr Phe Pro Asp Ala Asp Ala Asp Glu Asp Ser Leu Ala Gly Glu	
65 70 75 80	
ctg gat gag gcc atg ggg tcc agc gag tgg ctg gcc ctg acc aag tca	288
Leu Asp Glu Ala Met Gly Ser Ser Glu Trp Leu Ala Leu Thr Lys Ser	
85 90 95	
ccc cag gcc ttt tac agg ggg cga ccc agc tgg caa gga acc cct ggg	336
Pro Gln Ala Phe Tyr Arg Gly Arg Pro Ser Trp Gln Gly Thr Pro Gly	
100 105 110	
gtt ctt cg ^g ggc agc cga gat gtc ctg gct ggc ctt tcc agc agc tgc	384
Val Leu Arg Gly Ser Arg Asp Val Leu Ala Gly Leu Ser Ser Ser Cys	
115 120 125	
tgc aag tgg ggg tgt agc aaa agt gaa atc agt agc ctt tgc tag	429
Cys Lys Trp Gly Cys Ser Lys Ser Glu Ile Ser Ser Leu Cys *	
130 135 140	
<210> 2	
<211> 142	
<212> PRT	
<213> Homo sapiens	
<400> 2	
Met Ala Arg Tyr Met Leu Leu Leu Leu Leu Ala Val Trp Val Leu Thr	
1 5 10 15	
Gly Glu Leu Trp Pro Gly Ala Glu Ala Arg Ala Ala Pro Tyr Gly Val	
20 25 30	
Arg Leu Cys Gly Arg Glu Phe Ile Arg Ala Val Ile Phe Thr Cys Gly	
35 40 45	
Gly Ser Arg Trp Arg Arg Ser Asp Ile Leu Ala His Glu Ala Met Gly	
50 55 60	
Asp Thr Phe Pro Asp Ala Asp Ala Asp Glu Asp Ser Leu Ala Gly Glu	
65 70 75 80	
Leu Asp Glu Ala Met Gly Ser Ser Glu Trp Leu Ala Leu Thr Lys Ser	
85 90 95	
Pro Gln Ala Phe Tyr Arg Gly Arg Pro Ser Trp Gln Gly Thr Pro Gly	
100 105 110	

Val Leu Arg Gly Ser Arg Asp Val Leu Ala Gly Leu Ser Ser Ser Cys
115 120 125
Cys Lys Trp Gly Cys Ser Lys Ser Glu Ile Ser Ser Leu Cys
130 135 140

<210> 3
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Cysteine motif

<221> VARIANT
<222> (3)...(13)
<223> Each Xaa is independently any amino acid residue
except cysteine.

<400> 3
Leu Cys Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys
1 5 10

<210> 4
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Motif

<221> VARIANT
<222> (3)...(5)
<223> Each Xaa is independently any amino acid residue
except cysteine.

<221> VARIANT
<222> (4)...(14)
<223> Each Xaa is independently any amino acid residue
except cysteine.

<400> 4

Cys Cys Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys
 1 5 10 15

<210> 5

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Motif

<221> VARIANT

<222> (2)...(4)

<223> Each Xaa is independently any amino acid residue
 except cysteine.

<400> 5

Arg Xaa Xaa Xaa Arg
 1 5

<210> 6

<211> 426

<212> DNA

<213> Artificial Sequence

<220>

<223> Degenerate polynucleotide sequence encoding the
 polypeptide of SEQ ID NO:2.

<221> variation

<222> (1)...(426)

<223> Each N is independently A, T, G, or C.

<400> 6

atggcnmgnt	ayatgytnyt	nytnytnytn	gcngtntggg	tyntnacngg	ngarytntgg	60
ccnggngcng	argcnmgngc	ngcncntay	ggngtnmgny	tntgyggngm	ngarttyath	120
mgngcngtna	thttyacntg	yggnggnwsn	mgntggmgnm	gnwsngayat	hyngcncay	180
gargcnatgg	gngayacntt	yccngaygcn	gaygcngayg	argaywsnyt	ngcnggngar	240
ytngaygarg	cnatgggnws	nwsngartgg	ytngcnytna	cnaarwsncc	ncargcntty	300
taymgnggnm	gnccnwsntg	gcarggnacn	ccnggngtny	tnmgnggnws	nmngaygtn	360

ytngcngny tnwsnwsnws ntgytgyaar tgggntgyw snaarwsnga rathwsnwsn 420
ytntgy 426

<210> 7
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide ZC9736

<400> 7
ccataccct gaccctgtt gagat 25

<210> 8
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide ZC9740

<400> 8
cagaggttcc ctgataccca cacat 25

<210> 9
<211> 55
<212> DNA
<213> Artificial Sequence

<220>
<223> Exon 1 sense oligonucleotide primer

<400> 9
tgaagaaggt ctcgaattcg tcgacaccat ggccaggtac atgctgctgc tgctc 55

<210> 10
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Exon 1 antisense oligonucleotide primer

<400> 10
tgaagaagg t c t a c t c c a t a g c c t c g t g g g c c a g g a t g t c t g a 45

<210> 11
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Exon 2 sense oligonucleotide primer

<400> 11
t g a a g a a g g t c t c a g g a g a t a c c t t c c g g a t g c a g a t g c t 41

<210> 12
<211> 52
<212> DNA
<213> Artificial Sequence

<220>
<223> Exon 2 antisense oligonucleotide primer

<400> 12
t g a a g a a g g t c t c t c t a g a a a c t c t a g c a a a g g c t a c t g a t t c a c t t t t g c t 52

<210> 13
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> conserved motif

<221> VARIANT
<222> (1)...(4)
<223> Xaa = Any Amino Acid

<400> 13
A r g X a a X a a A r g
1